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SEQUENCE LISTING

<110> Pompejus, Markus
Doval, Jose Luis Revuelta
Garcia, Maria Angeles Santos

<120> Orotidine-5'-phosphate decarboxylase gene, gene construct comprising this gene and its use.

<140> US 09/582,779

<141> 2000-07-03

<150> Germany/19801120.2

<151> 1998-01-15

<160> 5

<170> WordPerfect version 6.1

<210> 1

<211> 1380

<212> DNA

<213> Ashbya gossypii

<220>

<221> CDS

<222> 210 ... 1013

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ctatcatgta tgctgtcact acagaaaaat ttttgtctat agctggcaag aagcacatca	120
catacattct gatggtgtag gctccacatc acagtaagca tttgtataag gctgatcaca	180
tagggtgcta ccgacctagc cattggcac atg tca acg aaa tct tac gca gaa	233
Met Ser Thr Lys Ser Tyr Ala Glu	
1 5	
agg gcc aag gca cac aat tgg cca gtt gct aga aag ctt ctg gca ttg	281
Arg Ala Lys Ala His Asn Ser Pro Val Ala Arg Lys Leu Leu Ala Leu	
10 15 20	
atg cac gag aag aaa acc aat ctc tgc gct tcc ctt gat gtg cgg acg	329
Met His Glu Lys Lys Thr Asn Leu Cys Ala Ser Leu Asp Val Arg Thr	
25 30 35 40	
tct aga aag ctt ctg gag cta gca gac acg ctg gga ccg cac att tgt	377
Ser Arg Lys Leu Leu Glu Leu Ala Asp Thr Leu Gly Pro His Ile Cys	
45 50 55	
ctg ctg aag aca cat gtc gac ata ctg acg gac ttc gac atc gag acg	425

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16

Leu Leu Lys Thr His Val Asp Ile Leu Thr Asp Phe Asp Ile Glu Thr
 60 65 70

aca gtc aag ccg ctg cag cag ctt gcg gct aag cac aac ttc atg atc 473
 Thr Val Lys Pro Leu Gln Gln Leu Ala Ala Lys His Asn Phe Met Ile
 75 80 85

ttc gag gac cgc aag ttc gct gac att ggc aac acg gtt aag ctg cag 521
 Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly Asn Thr Val Lys Leu Gln
 90 95 100

tac tcc tcc ggc gtg tac cgt atc gcg gag tgg gcg gat att acc aat 569
 Tyr Ser Ser Gly Val Tyr Arg Ile Ala Glu Trp Ala Asp Ile Thr Asn
 105 110 115 120

gca cac ggc gtc acc ggc ccc ggt gtg ata gcc ggg ctg aag gag gct 617
 Ala His Gly Val Thr Gly Pro Gly Val Ile Ala Gly Leu Lys Glu Ala
 125 130 135

gcg aaa ctg gcc tca cag gaa ccc agg ggg ttg ctg atg ctg gca gag 665
 Ala Lys Leu Ala Ser Gln Glu Pro Arg Gly Leu Leu Met Leu Ala Glu
 140 145 150

ctc tct tct cag ggc tct ttg gcg cgc gga gac tat acc gcg ggc gtc 713
 Leu Ser Ser Gln Gly Ser Leu Ala Arg Gly Asp Tyr Thr Ala Gly Val
 155 160 165

gtt gaa atg gcg aag ctg gac gaa gac ttt gtg atc ggg ttc atc gcg 761
 Val Glu Met Ala Lys Leu Asp Glu Asp Phe Val Ile Gly Phe Ile Ala
 170 175 180

cag cgt gac atg ggt ggg cgt gca gac ggc ttt gac tgg ctc atc atg 809
 Gln Arg Asp Met Gly Gly Arg Ala Asp Gly Phe Asp Trp Leu Ile Met
 185 190 195 200

acc ccg ggg gtt ggc ctg gac gac aaa gga gac ggc ctg ggc cag cag 857
 Thr Pro Gly Val Gly Leu Asp Asp Lys Gly Asp Gly Leu Gly Gln Gln
 205 210 215

tac cgc acg gtg gat gag gtc gtc agc gac ggt acc gat gtg atc att 905
 Tyr Arg Thr Val Asp Glu Val Val Ser Asp Gly Thr Asp Val Ile Ile
 220 225 230

gtt ggc aga ggg ctc ttt gac aag gga aga gac ccc aag gtc gag ggt 953
 Val Gly Arg Gly Leu Phe Asp Lys Gly Arg Asp Pro Lys Val Glu Gly
 235 240 245

gcc cgc tac cgc aag gcc ggt tgg gag gct tac ttg cgc cgt atg ggc 1001
 Ala Arg Tyr Arg Lys Ala Gly Trp Glu Ala Tyr Leu Arg Arg Met Gly
 250 255 260

gag act tcg tagtctatcg ctggcgccca cagtatatag gcggattcca 1050
 Glu Thr Ser

265

ccgccgatta ccattctcagc aacctttttg taattatatg cccctattgc ccttatttcc 1110
 gagctgggtgc cgggatcggg ttatagacgg gcaacaagtt gatactttgt tcagtagcat 1170
 gcatccaaca cttgcaggct tgggggtgtgg aaggcctcgc cgcggataat tcgtattacc 1230
 cgcacttcgt gaagtattgc tttatgaaaa atcttcactt tgggctaact agagccataa 1290
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<211> 267

<212> PRT

<213> Ashbya gossypii

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Val Ala Arg Lys Leu Leu Ala Leu Met His Glu Lys Lys Thr Asn Leu
 20 25 30

Cys Ala Ser Leu Asp Val Arg Thr Ser Arg Lys Leu Leu Glu Leu Ala
 35 40 45

Asp Thr Leu Gly Pro His Ile Cys Leu Leu Lys Thr His Val Asp Ile
 50 55 60

Leu Thr Asp Phe Asp Ile Glu Thr Thr Val Lys Pro Leu Gln Gln Leu
 65 70 75 80

Ala Ala Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala Asp
 85 90 95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ser Gly Val Tyr Arg Ile
 100 105 110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Pro Gly
 115 120 125

Val Ile Ala Gly Leu Lys Glu Ala Ala Lys Leu Ala Ser Gln Glu Pro
 130 135 140

Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Gln Gly Ser Leu Ala
 145 150 155 160

Arg Gly Asp Tyr Thr Ala Gly Val Val Glu Met Ala Lys Leu Asp Glu

165

170

175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Ala
 180 185 190

Asp Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
 195 200 205

Lys Gly Asp Gly Leu Gly Gln Gln Tyr Arg Thr Val Asp Glu Val Val
 210 215 220

Ser Asp Gly Thr Asp Val Ile Ile Val Gly Arg Gly Leu Phe Asp Lys
 225 230 235 240

Gly Arg Asp Pro Lys Val Glu Gly Ala Arg Tyr Arg Lys Ala Gly Trp
 245 250 255

Glu Ala Tyr Leu Arg Arg Met Gly Glu Thr Ser
 260 265

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<211> 18

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1 ... 18

<400> 3

ytnggncnt ayathtgy

<210> 4

<211> 23

<212> DNA

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<222> 1 ... 23

<400> 4

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<210> 5

<211> 26


<212> DNA

<213> Artificial sequence

<220>
<221> misc_feature
<222> 1 ... 26

<400> 5

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<211> 19
<212> DNA
<213> Artificial sequence

<220>
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<400> 6

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